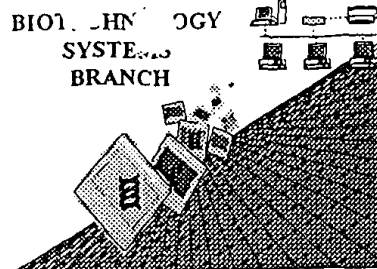
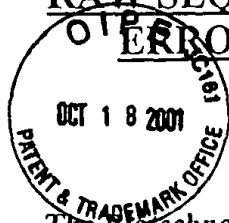


Sorbell



#11
7-26-0
P2

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/515,369A
Source: 1633
Date Processed by STIC: 7-5-01

RECEIVED

JUL 25 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

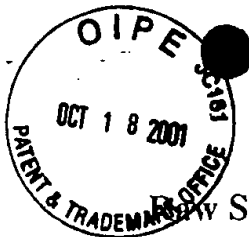
Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>



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JUL 25 2001

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Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTIONSERIAL NUMBER: 09/515,369A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
 Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
 prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
 Numbering use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
 ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules,
 each n or Xaa can only represent a single residue. Please present the maximum number of each
 residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
 "bug" sequences(s) . Normally, PatentIn would automatically generate this section from the
 previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
 the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
 Artificial or Unknown sequences.
- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 (NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 9 ✓ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
 (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
 Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
 is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
 "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
 "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
 listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.



RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/515,369A

DATE: 07/05/2001

TIME: 12:54:49

Input Set : A:\56778.txt

Output Set : N:\CRF3\07032001\I515369A.raw

3 <110> APPLICANT: Fisher, Paul
 4 Madireddi, Malavi
 6 <120> TITLE OF INVENTION: MELANOMA DIFFERENTIATION ASSOCIATED GENE-7 PROMOTER AND USES
 THEREOF

8 <130> FILE REFERENCE: 0575/56778/JPW/APE
 10 <140> CURRENT APPLICATION NUMBER: 09/515,369A
 11 <141> CURRENT FILING DATE: 2000-02-29
 13 <160> NUMBER OF SEQ ID NOS: 13
 15 <170> SOFTWARE: PatentIn version 3.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 2286
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Human
 22 <400> SEQUENCE: 1

Does Not Comply
 Corrected Diskette Needed

See p. 4

23	taatacgact	cactataggg	cgtcgactcg	atcacctttt	gaacccaggt	ctgcctgcct	60
25	ccaaagcttg	tactcataac	tagattctca	actgatgttg	ggccaagggt	cctaggttct	120
27	ctccttgacc	tcccttctga	agtaataatg	ctatgataag	ctcatcgag	gctgaggccc	180
29	aggcacatgt	tgcctgaac	tatccatggt	atatgattcc	ttcctcagac	agagtgaagt	240
31	actcacgac	ccaggtgtac	cctgaggcca	gccaagggtg	atccatgacc	tcatgcctct	300
33	gttccagcct	gccctttaac	agctcatccc	acctgcctgc	cctccccgcc	tatctgcaga	360
35	cagtagtota	ggatttcagc	tgccctgggg	gtcatttttc	cctctcagct	tcctgcttta	420
37	gctgtctect	gcctcccaact	cacctattac	tccagcactc	tcacctggtc	ttcttttctg	480
39	tctcatcact	gcctcttgac	atctttatct	catagtagtt	agttaggggt	tcttggtaat	540
41	gcctaaatc	cacatggttg	gaagggggga	gtgggggaag	agagtgcgct	gtggggctgt	600
43	gcctacttct	ggagggtgag	actcggggcc	tccagggaac	aaggattcag	gctggtggca	660
45	gctatagcca	agcagactgc	tggccaggga	ttgcaaagga	gtattttgtt	tgcttaagaa	720
47	aataaacaac	actgagtagt	agatggaggg	aggggggtgt	ggtgccagag	agattgggaa	780
49	gagtctgcca	agggtgtgtt	ctactcaact	tcctcttttc	tttcatctcc	actgagctgg	840
51	aggcagttat	cctgtccccc	acgtcacatt	cctactcccg	tttcccatgc	ctggacccag	900
53	gttggggcaa	ctcttctgt	aaagaaccag	acaggaaacta	ttttaggctc	tgtgtgccaat	960
55	atggtctcag	tcacaactac	tcactctctg	ctctgtagca	cgaaagcaat	tagcaacaat	1020
57	atgtcaacaa	acatatgtga	ccccatgaaa	actttattta	ttatggatac	ggaaacctga	1080
59	aaataatgtc	tttcttttga	ttttttcccc	aatcattaaa	aaacgtaaaa	actactctta	1140
61	ggtcgcaagg	ttaagccatt	ctcagcttag	cagtggcagg	ctggatttgg	cttgtgacct	1200
63	acagttggcc	aatccctgat	tcccaaaatg	tattcctcag	ggatgtgggc	aaatacttat	1260
65	gggaagtgtc	ggattaaaca	gagttaagaa	gcacagaca	tttccaggac	gggctagcac	1320
67	atgccagggc	tctctaaact	acctcattgg	attcatctgt	ttcatggagg	atcttgcaag	1380
69	acaagaattc	ctcaaaccta	gagtctgagg	actgtgcttt	gggaaacact	gctctgcttg	1440
71	atgccctcac	tgggcacatg	gtagaatcta	gagctgagtg	ccttgctagc	tggagatagg	1500
73	gtcagagctc	ttgactgccc	tggcagtctt	gacacatcac	gctgtctgtg	tcacctgagt	1560
75	ggttcagagc	cacacaggcc	aagactagcc	caccagagca	ccaggcctcc	cagctttctg	1620
77	ggcttgctcca	tgcgtacatt	tccttattct	tcctggtttc	cagaacctaa	ggagaggcac	1680
79	attttggttg	agtgattata	accctaggga	ccatgggtag	ctgcatgtca	ggaaacactc	1740
81	ctcaacttcc	tggccctgat	ggattaaagg	agaggtaact	acaggttatt	tcttcgctgt	1800
83	ggactactgt	cccagcatga	atagggcatc	attattgaat	tattttgaca	ggaaggagac	1860
85	tgggtgatgc	tgcacagtaa	taatgtatct	acatgtgtac	agagtttacc	aagcacctct	1920
87	gtgttggttt	tgcctttgtt	tattacactt	gggacaaatt	tttaaaattt	atacatgcag	1980
89	agactgcagc	gcagagaagc	taagagactt	gccctgccc	acacagccag	tggtagagcc	2040

RAW SEQUENCE LISTING

DATE: 07/05/2001

PATENT APPLICATION: US/09/515,369A

TIME: 12:54:49

Input Set : A:\56778.txt

Output Set: N:\CRF3\07032001\I515369A.raw

```

91 tgaactcaaa cccaggtctc atctcacctc aggggctgct ttccccatcg ctgtattgtc 2100
93 cttaaagtga tgggtgacta ggcaatgaag taattctcta ggaaagcatg accaatttcc 2160
95 ctttctccac ctccctcttt ttctccacc cctcccccat cagcccccat atatatgcc 2220
97 aaatctccac aaagccttgc ttgctgcaa acctttactt ctgaaatgac ttccacggct 2280
99 gggacg 2286
102 <210> SEQ ID NO: 2
103 <211> LENGTH: 21
104 <212> TYPE: DNA
105 <213> ORGANISM: Artificial Sequence
107 <220> FEATURE:
108 <221> NAME/KEY: misc_feature
109 <222> LOCATION: ()..()
110 <223> OTHER INFORMATION: primer
113 <400> SEQUENCE: 2
114 cgtccagcc gtggaagtca t 21
117 <210> SEQ ID NO: 3
118 <211> LENGTH: 21
119 <212> TYPE: DNA
120 <213> ORGANISM: Artificial Sequence
122 <220> FEATURE:
123 <221> NAME/KEY: misc_feature
124 <222> LOCATION: ()..()
125 <223> OTHER INFORMATION: primer
128 <400> SEQUENCE: 3
129 aggctggatt tggcttgtga c 21
132 <210> SEQ ID NO: 4
133 <211> LENGTH: 21
134 <212> TYPE: DNA
135 <213> ORGANISM: Artificial Sequence
137 <220> FEATURE:
138 <221> NAME/KEY: misc_feature
139 <222> LOCATION: ()..()
140 <223> OTHER INFORMATION: primer
143 <400> SEQUENCE: 4
144 ctgtttaatc cagcacttcc c 21
147 <210> SEQ ID NO: 5
148 <211> LENGTH: 21
149 <212> TYPE: DNA
150 <213> ORGANISM: Artificial Sequence
152 <220> FEATURE:
153 <221> NAME/KEY: misc_feature
154 <222> LOCATION: ()..()
155 <223> OTHER INFORMATION: primer
158 <400> SEQUENCE: 5
159 cgcttgatga ctacgccga a 21
162 <210> SEQ ID NO: 6
163 <211> LENGTH: 20
164 <212> TYPE: DNA
165 <213> ORGANISM: Artificial Sequence

```

RAW SEQUENCE LISTING

DATE: 07/05/2001

PATENT APPLICATION: US/09/515,369A

TIME: 12:54:49

Input Set : A:\56778.txt

Output Set: N:\CRF3\07032001\I515369A.raw

```

167 <220> FEATURE:
168 <221> NAME/KEY: misc_feature
169 <222> LOCATION: ()..()
170 <223> OTHER INFORMATION: primer
173 <400> SEQUENCE: 6
174 tgcagattgc gcaatctgca 20
177 <210> SEQ ID NO: 7
178 <211> LENGTH: 21
179 <212> TYPE: DNA
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <221> NAME/KEY: misc_feature
184 <222> LOCATION: ()..()
185 <223> OTHER INFORMATION: primer
188 <400> SEQUENCE: 7
189 cgcttgatga cttggccgga a 21
192 <210> SEQ ID NO: 8
193 <211> LENGTH: 22
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <221> NAME/KEY: misc_feature
199 <222> LOCATION: ()..()
200 <223> OTHER INFORMATION: primer
203 <400> SEQUENCE: 8
204 tgcagagaga ctagtctctg ca 22
207 <210> SEQ ID NO: 9
208 <211> LENGTH: 61
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <221> NAME/KEY: misc_feature
214 <222> LOCATION: ()..()
215 <223> OTHER INFORMATION: primer
218 <400> SEQUENCE: 9
219 uuguauuuau uacaacucua uuuaauuuau gucaguauuu caacugaagu ucuauuuauu 60
221 u 61
224 <210> SEQ ID NO: 10
225 <211> LENGTH: 15
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <221> NAME/KEY: misc_feature
231 <222> LOCATION: ()..()
232 <223> OTHER INFORMATION: primer
235 <400> SEQUENCE: 10
236 uauuuauuuu uuuaa 15
239 <210> SEQ ID NO: 11
240 <211> LENGTH: 51

```

RAW SEQUENCE LISTING

DATE: 07/05/2001

PATENT APPLICATION: US/09/515,369A

TIME: 12:54:49

Input Set : A:\56778.txt

Output Set: N:\CRF3\07032001\I515369A.raw

241 <212> TYPE: DNA
 242 <213> ORGANISM: Artificial Sequence
 244 <220> FEATURE:
 245 <221> NAME/KEY: misc_feature
 246 <222> LOCATION: ()..()
 247 <223> OTHER INFORMATION: primer
 250 <400> SEQUENCE: 11
 251 uauuuuuuuu uauuuuuuuu uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu a 51
 254 <210> SEQ ID NO: 12
 255 <211> LENGTH: 38
 256 <212> TYPE: DNA
 257 <213> ORGANISM: Artificial Sequence
 259 <220> FEATURE:
 260 <221> NAME/KEY: misc_feature
 261 <222> LOCATION: ()..()
 262 <223> OTHER INFORMATION: primer
 265 <400> SEQUENCE: 12
 W--> 266 suncauuuuu uauuuuuuuu uuuuuuuuuu uuuuuuuu 38
 269 <210> SEQ ID NO: 13
 270 <211> LENGTH: 56
 271 <212> TYPE: DNA
 272 <213> ORGANISM: Artificial Sequence
 274 <220> FEATURE:
 275 <221> NAME/KEY: misc_feature
 276 <222> LOCATION: ()..()
 277 <223> OTHER INFORMATION: primer
 280 <400> SEQUENCE: 13
 281 guuuuuuuuu uuuuuuuuuu gauggauucu cagauuuuuu uuuuuuuuuu uuauuu 56

Sequence #12 is missing the
 mandatory <220> to <223> features
 to explain the "n" in the sequence
 See #9 on the Error Summary
 Sheet.

VERIFICATION SUMMARY

DATE: 07/05/2001

PATENT APPLICATION: US/09/515,369A

TIME: 12:54:50

Input Set : A:\56778.txt

Output Set: N:\CRF3\07032001\I515369A.raw

L:266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12